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GenCore version 5.1.6

run on: July 29, 2004, 13:38:08 ; Search time 57 Seconds
(without alignments)

protein - Protein search, using sw model

Sequence: 7401.817 Million cell updates/sec

title: US-10-090-183-6

target score: 7046

Sequence: 1 MESKALLAVALMPCVETRAA.....KMDVDAVHADSGTTLRSPPV 1345

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 1291235 seqs, 313382936 residues

total number of hits satisfying chosen parameters: 1291235

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

database : Published Applications AA:*

1: /cgn2_6_ptodata/2_pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6_ptodata/2_pubpaa/PCT_NEW_PUB.pep:*

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18: /cgn2_6_ptodata/2_pubpaa/US60_PUBCOMB.pep:*

RESULT 1
US-10-090-183-6

; Application US-10090183

; Publication No. US20030185802A1

; GENERAL INFORMATION:

; APPLICANT: The Scripps Research Institute

; APPLICANT: Ralph A. Reisfeld

; APPLICANT: Andrew G. Niethammer

; APPLICANT: Rong Xiang

; TITLE OF INVENTION: DNA VACCINE AGAINST PROLIFERATING ENDOTHELIAL CELLS AND METHODS OF USE THEREOF

; FILE REFERENCE: TSRI-829.0

; CURRENT APPLICATION NUMBER: US10/090,183

; CURRENT FILING DATE: 2002-03-02

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 1345

; TYPE: PRT

; ORGANISM: mouse

US-10-090-183-6

Query Match Score 7046; DB 14; Length 1345;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1345; Conservative 0; Missmatches 0;

Sequence 6, Appli

Sequence 2, Appli

Sequence 10, Appli

Sequence 6, Appli

Sequence 6, Appli

Sequence 2, Appli

Sequence 2, Appli

Sequence 6, Appli

Sequence 6, Appli

Sequence 11, Appli

Sequence 2, Appli

Sequence 66, Appli

Sequence 129, Appli

Sequence 7, Appli

Sequence 19, Appli

Sequence 8, Appli

Sequence 34, Appli

Sequence 215, Appli

Sequence 23, Appli

Sequence 44, Appli

Sequence 84, Appli

Sequence 26, Appli

Sequence 4, Appli

Sequence 129, Appli

Sequence 33, Appli

Sequence 9, Appli

Sequence 2, Appli

Sequence 4, Appli

Sequence 2, Appli

Sequence 33, Appli

Sequence 2, Appli

Sequence 32, Appli

Sequence 67, Appli

Sequence 5, Appli

ALIGNMENTS

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	7046	100.0	1345	14	US-10-090-183-6	Sequence 6, Appli
2	7020	99.6	1367	9	US-09-766-678-2	Sequence 2, Appli
3	7020	99.6	1367	15	US-10-165-193A-10	Sequence 10, Appli
4	6984	99.3	1367	9	US-09-919-108-6	Sequence 6, Appli
5	6984	99.3	1367	9	US-09-87-136-6	Sequence 6, Appli
6	6127.5	87.0	1356	14	US-10-022-939-2	Sequence 2, Appli
7	6127.5	87.0	1356	14	US-10-100-405A-2	Sequence 2, Appli
8	6127.5	87.0	1356	14	US-10-327-414-6	Sequence 6, Appli
9	6127.5	87.0	1356	15	US-10-165-193A-11	Sequence 11, Appli
10	6124.5	86.9	1356	14	US-10-090-183-2	Sequence 2, Appli
11	6124.5	86.9	1356	15	US-10-394-322A-66	Sequence 66, Appli
12	6124.5	86.9	1356	15	US-10-440-464-129	Sequence 129, Appli
13	6123.5	86.9	1356	10	US-09-969-037-7	Sequence 7, Appli
14	6092.5	86.5	1354	14	US-10-52538-30	Sequence 5, Appli
15	4228	60.0	806	9	US-09-766-678-5	Sequence 5, Appli

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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:35:17 ; Search time 23 Seconds (without alignments)

Scoring table: BLOSUM62 , Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0*
Maximum Match 100*
Listing first 45 summaries

Database : Issued_Patent's AA:
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3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep:
5: /cgn2_6/prodata/2/iaa/8CTUS_COMB.pep:
6: /cgn2_6/prodata/2/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	7020	99.6	1367	2	US-08-443-861-2		Sequence 2, Appli
2	7020	99.6	1367	3	US-08-493-89B-2		Sequence 2, Appli
3	6994	99.3	1367	1	US-07-813-533-4		Sequence 4, Appli
4	6994	99.3	1367	1	US-07-977-451-6		Sequence 6, Appli
5	6994	99.3	1367	1	US-07-946-507-4		Sequence 4, Appli
6	6994	99.3	1367	1	US-08-552-517-6		Sequence 6, Appli
7	6994	99.3	1367	1	US-07-906-39TA-6		Sequence 6, Appli
8	6994	99.3	1367	1	US-08-001-891-6		Sequence 6, Appli
9	6994	99.3	1367	2	US-09-021-324-6		Sequence 6, Appli
10	6994	99.3	1367	4	US-09-871-136B-6		Sequence 6, Appli
11	6994	99.3	1367	5	PCT-US200202750-8		Sequence 8, Appli
12	6994	99.3	1367	5	PCT-US2002-05401-6		Sequence 6, Appli
13	6994	99.3	1367	5	PCT-US2002-05993-6		Sequence 6, Appli
14	6127.5	87.0	1356	3	US-09-098-707A-2		Sequence 2, Appli
15	6127.5	87.0	1356	4	US-09-0483-539-2		Sequence 2, Appli
16	6102.5	86.5	1356	1	US-08-810-116-8		Sequence 8, Appli
17	6102.5	86.5	1356	2	US-07-330-548A-8		Sequence 8, Appli
18	4228	60.0	806	2	US-08-443-861-5		Sequence 5, Appli
19	4228	60.0	806	3	US-08-193-829B-5		Sequence 5, Appli
20	4196	59.6	805	3	US-08-385-526-34		Sequence 34, Appli
21	3327.5	47.2	788	1	US-08-332-538-15		Sequence 15, Appli
22	3327.5	47.2	788	2	US-08-786-164-15		Sequence 15, Appli
23	3248	46.1	764	4	US-08-442-946B-14		Sequence 14, Appli
24	3245	46.1	767	2	US-08-874-678-2		Sequence 2, Appli
25	3245	46.1	767	3	US-08-843-839-2		Sequence 2, Appli
26	3245	46.1	767	4	US-09-348-886-2		Sequence 2, Appli
27	2792	39.6	668	2	US-08-786-164-13		Sequence 13, Appli
28	2792	39.6	1368	2	US-08-874-678-34		Sequence 34, Appli
29	2733.5	38.8	1368	3	US-08-643-839-4		Sequence 34, Appli
30	2733.5	38.8	1368	4	US-09-348-886-34		Sequence 34, Appli
31	2733.5	38.8	1338	3	US-08-750-141A-3		Sequence 3, Appli
32	2694.5	38.2	1338	4	US-09-119-014D-6		Sequence 6, Appli
33	2694.5	38.2	1362	2	US-08-874-678-33		Sequence 33, Appli
34	2691.5	38.2	1362	3	US-08-643-839-33		Sequence 33, Appli
35	2691.5	38.2	1362	4	US-09-348-886-33		Sequence 33, Appli
36	2691.5	38.2	1363	1	US-08-340-011-4		Sequence 4, Appli
37	2682	38.1	1363	3	US-08-901-710-4		Sequence 4, Appli
38	2682	38.1	1298	1	US-08-122-616-33		Sequence 33, Appli
39	2677.5	38.0	1298	1	US-08-340-011-2		Sequence 2, Appli
40	2677.5	38.0	1298	3	US-08-901-710-2		Sequence 33, Appli
41	2677.5	38.0	1298	4	US-08-446-648-33		Sequence 33, Appli
42	2677.5	38.0	1298	4	US-09-982-610-33		Sequence 33, Appli
43	2677.5	38.0	1298	5	PCT-US95-04228-33		Sequence 33, Appli
44	2677.5	38.0	1311	1	US-08-340-011-5		Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-443-861-2
; Sequence 2, Application US/08443861
; Patent No. 585199
; GENERAL INFORMATION:
/ APPLICANT: Ullrich, Axel
/ APPLICANT: Riesau, Werner
/ APPLICANT: Millauer, Birgit
/ APPLICANT: Gazit, Aviv
/ APPLICANT: Levitzki, Alex
TITLE OF INVENTION: FLK-1 Is A Receptor For Vascular
TITLE OF INVENTION: Endothelial Growth Factor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie S. Edmonds
STREET: 11036 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443, 861
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/193, 829
REFERENCE/DOCKET NUMBER: 7683-060
FILING DATE: 09-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30, 742
TELEPHONE: (212) 790-9090
TELEFAX: (212) 669-9741
TELEFAX: (661) 441 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1367 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-443-861-2

Query Match Similarity 99.6% ; Score 7020; DB 2; Length 1367;
Best Local Similarity 99.9%; Pred. No. 0;

macrophage colony	30	990.5	14.1	972	1	TVHUMD
c-kit-related kina	31	989.5	14.0	954	2	I51703
fibroblast growth	32	989	14.0	822	2	I49289
fibroblast growth	33	985	14.0	822	1	TVHUFG
fibroblast growth	34	984	14.0	821	1	TVHUF2
fibroblast growth	35	984	14.0	832	2	JH0393
fibroblast growth	36	981	13.9	822	1	TVMSPG
fibroblast growth	37	980.5	13.9	941	1	TVMVMD
protein-tyrosine k	38	976.5	13.9	812	1	A36477
fibroblast growth	39	974.5	13.8	820	2	S17295
fibroblast growth	40	974.5	13.8	822	2	A45081
fibroblast growth	41	973.5	13.8	822	2	B54846
fibroblast growth	42	972.5	13.8	823	2	B35963
protein-tyrosine k	43	972	13.8	822	2	S29849
fibroblast growth	44	966.5	13.7	822	2	A41794
keratinocyte growth	45	962	13.7	729	2	A56795
						ALIGNMENTS
						RESULT 1
						A41228
						protein-tyrosine kinase (EC 2.7.1.112) Flk-1 precursor, endothelial cell-specific
						C;Species: Mus musculus (house mouse)
						C;Date: 19-Jun-1992 #sequence revision 19-Jun-1992 #text_change 04-Feb-2000
						C;Accession: A41228; A46065; T58365; S18832; S29991
						R;Matthews, W.; Jordan, C.T.; Gavin, M.; Jenkins, N.A.; Copeland, N.G.; Lemisch, A.
						Proc. Natl. Acad. Sci. U.S.A. 88, 9026-9030, 1991
						A;Title: A receptor tyrosine kinase cDNA isolated from a population of enriched
						A;Reference number: A41228; MUID:93208880; PMID:1717995
						A;Accession: A41228
						A;Status: preliminary
						A;Molecule type: mRNA
						A;Residues: 1-1367 <MAT>
						A;Cross-references: GB:X559397; NID:G50976; PID:CRN42040.1; PID:G50977
						R;Müller, B.; Wizemann-Voos, S.; Schnurch, H.; Martinez, R.; Möller, N.P.; R.
						Cell 72, 835-846, 1993
						A;Title: High affinity VEGF binding and developmental expression suggest Flk-1.
						A;Accession number: A46065; MUID:93208880; PMID:1717995
						A;Accession: A46065
						A;Status: preliminary; not compared with conceptual translation
						A;Molecule type: mRNA
						A;Residues: 1-24, 'T', '26-782', 'VL', '785-916', 'C', '918-1367 <ML>
						A;Cross-references: GB:X70842; NID:G51923; PID:CRN450192.1; PID:957924
						A;Note: submitted to the EMBL Data Library, January 1993
						A;Note: sequence extracted from NCBI backbone (NCBIP:128064)
						R;Oelrichs, R.B.; Reid, H.H.; Bernard, O.; Ziemicke, A.; Wilks, A.F.
						Oncogene 8, 11-18, 1993
						A;Title: NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from E
						A;Reference number: 156365; MUID:9314125; PMID:823988
						A;Accession: 158365
						A;Status: preliminary; translated from GB/EMBL/DDJB
						A;Molecule type: mRNA
						A;Residues: 1-678, 'D', '680-1340', RSPPV, <OEL>
						A;Cross-references: GB:S53103; NID:9264004; PID:9264005
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						A;Gene: FLK-1; NYK
						C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinases; phosphotransferase; trans
						C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; kinase homology <KIN>
						P;I330-1165/Domain: protein kinase ATP-binding motif
						P;I338-846/Region: protein kinase ATP-binding motif
						Query Match Best Local Similarity Score DB 2; Length 1367;
						Matches 1336; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy						1 MESSKALAYVALWFCVETRAASVGLTGDFLHPPKLSLSTQKDILTLANTTLQITCRGQRDLD 60
Db						1 MESSKALAYVALWFCVETRAASVGLFGDFLHPPKLSLSTQKDILTLANTTLQITCRGQRDLD 60
Qy						1 MLLWNNAQRQSERERLVLTECGGDSIPCRILIPRUVNGNDGAKYC53YRDVIASTIVIV 120

Db	61 WLWPNQDSEERVLVTECGGDSIFCKTLTIPRVVGNDTGAYKCSYRVDIASTVVYV 120	Qy 1.201 EEEEVCDPKHYDNTAGISHYLLQNSKRSKSPVSVYKTFEDIPLEFPPVYV1PDDSDQTDSGM 1260
Qy	121 RDYRSPTASVSDQHGTIVYITENKNTKTVIPCRGSISNLNTSLCARYPERFVDPGNRIS 180	Db 1201 EEEEVCDPKHYDNTAGISHYLLQNSKRSKSPVSVYKTFEDIPLEFPPVYV1PDDSDQTDSGM 1260
Db	121 RDYRSPTASVSDQHGTIVYITENKNTKTVIPCRGSISNLNTSLCARYPERFVDPGNRIS 180	Qy 1261 VLASEEFLKTLEDRKNLSPSFGMMPSKSRSVASEGGSNQTSGYQGGHSSDDTDTVYSSD 1320
Qy	181 WDSEIGFTLPSMTSIYAGMVRCEAKINDETYQSIMIVVYGYRIVDVLSPPHETELSA 240	Db 1261 VLASEEFLKTLEDRKNLSPSFGMMPSKSRSVASEGGSNQTSGYQGGHSSDDTDTVYSSD 1320
Db	181 WDSEIGFTLPSMTSIYAGMVRCEAKINDETYQSIMIVVYGYRIVDVLSPPHETELSA 240	Qy 1321 EAGLIRKMDAIVHADSGRTTLR 13411
Qy	241 GEKLVNLNCTARTELNVGLDFTHSPSKSHHKCIVNDVKPPGTAVKMFSLTLESTV 300	Db 1321 EAGLIRKMDAIVHADSGRTTLQ 13411
Db	241 GEKLVNLNCTARTELNVGLDFTHSPSKSHHKCIVNDVKCFPPGTAVKMFSLTLESTV 300	Qy RESULT 2
Qy	301 KSDQGEBTCAVSSGRMKRNRIFEVVHTKPFIAFGSMKSLVBEATGYSQVRIPVCLSYV 360	Db JC1402 protein-tyrosine kinase (EC 2.7.1.112) KDR - human
Db	301 KSDQGEBTCAVSSGRMKRNRIFEVVHTKPFIAFGSMKSLVBEATGYSQVRIPVCLSYV 360	Qy C;Species: Homo sapiens (man)
Qy	361 ADPIKWTNRNGRPLESNYTMIVGDELTMINTERDAGNYTIVLTPNPSMEKQSHMVSIVNN 420	Db C;Date: 30-Sep-1993 #sequence_revision 28-Aug-1998 #text_change 04-Feb-2000
Db	361 ADPIKWTNRNGRPLESNYTMIVGDELTMINTERDAGNYTIVLTPNPSMEKQSHMVSIVNN 420	Qy C;Accession: JC1402; I58357
Qy	421 VPPQIGEKAALISPMDSYQGMYQGMYQGMYQGMYQGMYQGMYQGMYQGMYQGMYQ 480	Db R;Terman, B.I.; Dagher-Vermazen, M.; Carrion, M.E.; Dimitrov, D.C.; Artellino, D.C.; Gospk Biochem. Biophys. Res. Commun. 187, 1579-1586, 1992
Db	421 VPPQIGEKAALISPMDSYQGMYQGMYQGMYQGMYQGMYQGMYQGMYQGMYQGMYQ 480	Qy A;Title: Identification of the KDR tyrosine kinase as a receptor for vascular endothelia
Qy	481 KEWRHVEDFQGQNKIEVTKNQALIEGKNTVSTLVIQANVSYCEANKRGERV 540	Db A;Reference number: JCL402; PMID:93038639; PMID:1417831
Db	481 KEWRHVEDFQGQNKIEVTKNQALIEGKNTVSTLVIQANVSYCEANKRGERV 540	Qy A;Accession: JC1402
Qy	541 ISFHVTRGPEITVQPAQOPTEQESVSLCTADRNTPENLTWYKLGOATSVHMGESLTPV 600	Db A;Status: nucleic acid sequence not shown
Db	541 ISFHVTRGPEITVQPAQOPTEQESVSLCTADRNTPENLTWYKLGOATSVHMGESLTPV 600	Qy A;Molecule type: mRNA
Qy	601 CKNLDALWKLNQTMFSNSTNDLILIVAFONASLQDQGDYVCSAQDKTCKRHLCKVQIL 660	Db A;Cross-references: GB/EMBL/DDBJ
Db	601 CKNLDALWKLNQTMFSNSTNDLILIVAFONASLQDQGDYVCSAQDKTCKRHLCKVQIL 660	Qy C;Comment: This enzyme acts as a receptor for vascular endothelial cell growth factor.
Qy	661 ERMAPMTGQNLENQNTTGTIGETEVTCPASGNPPHTWFKDNETLVEDSGITVLRDGNRNL 720	Db A;Gene: G0B; KDR
Db	661 ERMAPMTGQNLENQNTTGTIGETEVTCPASGNPPHTWFKDNETLVEDSGITVLRDGNRNL 720	Qy A;Cross-references: GDB:127921; OMIM:191306
Qy	721 TIRRVRKEDGGLYTCAOCNVLGCAARETFILEGAQETKNTLLEVLTGAVIAMFFWLL 780	Db A;Map position: 4q12-4q12
Db	721 TIRRVRKEDGGLYTCAOCNVLGCAARETFILEGAQETKNTLLEVLTGAVIAMFFWLL 780	Qy C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
Qy	781 V1VLRVTKRANESELKGTYLSTIMDPELPLDRCERLPLDASKWEPFDRKLKGPKLGR 840	Db P;766-790/Domain: transmembrane protein; tyrosine-specific protein kinase
Db	781 V1VLRVTKRANESELKGTYLSTIMDPELPLDRCERLPLDASKWEPFDRKLKGPKLGR 840	Qy F;832-116/Domain: protein kinase homology <KIN>
Qy	841 GAFGQVIBADAFGIDKTTATCKTIVAKMVLREGATHSEIRALMELKLIIGHHLNTNL 900	Db P;840-848/Region: protein kinase ATP-binding motif
Db	841 GAFGQVIBADAFGIDKTTATCKTIVAKMVLREGATHSEIRALMELKLIIGHHLNTNL 900	Qy Query Match 86.6%; Score 6102.5; DB 2; Length 1356;
Qy	901 GACTKPGSPMLTYVECKFGNLSITYLCKRNEFVYPKSKGARFQKDYVGLSVDLKR 960	Db Best Local Similarity 85.4%; Pred. No. 2.1e-162; Matches 111; Indels 15; Gaps 3;
Db	901 GACTKPGSPMLTYVECKFGNLSITYLCKRNEFVYPKSKGARFQKDYVGLSVDLKR 960	Qy 1 MESKALLAVALWFCVTRAASVGLTQDILTLANTTLQITCRGQRDLD 60
Qy	961 LDSITSSOSASSGFVEKSLSDVEEEASELYKDFTELEHJJCYSFQVAKGMEFLASR 1020	Db 1 MESKVLAVALWLCVTRAASVGLPVSVDLPLRSLQDILTIKANTTLQITCRGQRDLD 60
Db	961 LDSITSSOSASSGFVEKSLSDVEEEASELYKDFTELEHJJCYSFQVAKGMEFLASR 1020	Qy 61 WLWPNQDSEERVLVTECGGDSFICKTLLTIPRIVGNDTGAYKCSYRVDIASTVVYV 120
Qy	1021 KCTHRLAARNLILSEKQVVKC1CDFGMLRDIYKDPDVYRKGDARLPLKWMAPTFIRVY 1080	Db 61 WLWPNQDSEERVLVTECGGDSFICKTLLTIPRIVGNDTGAYKCSYRVDIASTVVYV 120
Db	1021 KCTHRLAARNLILSEKQVVKC1CDFGMLRDIYKDPDVYRKGDARLPLKWMAPTFIRVY 1080	Qy 61 WLWPNQSGSRQVETEC--SDGLICKTLLTIPKQVGNQDTCAYKCYRETDLASVIVVV 118
Qy	1081 TIOSDWSFQVILWIFSLGASDYPGKIDDEFCRRLKEGTMRAPDTPEMYQMLDC 1140	Db 121 RDYRSPIASVSDQHGTIVYITENKNTVYICRGTSISNLNVLCAVYPERKFPVDPNRS 180
Db	1081 TIOSDWSFQVILWIFSLGASDYPGKIDDEFCRRLKEGTMRAPDTPEMYQMLDC 1140	Qy 119 QDYRSPIASVSDQHGTIVYITENKNTVYICRGTSISNLNVLCAVYPERKFPVDPNRS 178
Qy	1141 WHEDPNQRPSFSELEHNLQANQDGYDYLPMSETSMEDGSLSLPTSPVSCM 1200	Db 181 WDSEIGFTLPSYMSIAGMVFCEAKNDETYQSIMIVVYGYRIVDVLSPHETELSA 240
Db	1141 WHEDPNQRPSFSELEHNLQANQDGYDYLPMSETSMEDGSLSLPTSPVSCM 1200	Qy 179 WDSKKGCTIPSPMSIAGMVFCEAKNDESTQIMIVVYGYRIVDVLSPHETELSA 238
Qy	1141 WHEDPNQRPSFSELEHNLQANQDGYDYLPMSETSMEDGSLSLPTSPVSCM 1200	Db 241 GRKLVINVNTARTELNVGLDFTHSPSKSHHKCIVNDVKPPGTAVKMFSLSTLTSVT 300
Db	1141 WHEDPNQRPSFSELEHNLQANQDGYDYLPMSETSMEDGSLSLPTSPVSCM 1200	Qy 239 GEKLVINVNTARTELNVGIDENWBYPSKSHHKCIVNDVKPPGTAVKMFSLSTLTDGVT 298

Protein search results for the query sequence: MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345					
Search parameters: US-10-090-183-6					
Search time: 61 Seconds (without alignments)					
Total number of hits satisfying chosen parameters: 1586107					
Result No.	Score	Query	Length	DB	ID
1	7046	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
2	7020	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
3	6994	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
4	6994	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
5	6994	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
6	6994	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
7	6994	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
8	6994	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
9	6994	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
10	6994	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
11	6994	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
12	6994	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
13	6988	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
14	6980	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
15	6967	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
16	6124.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
17	6124.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
18	6124.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
19	6124.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
20	6124.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
21	6123.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
22	6123.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
23	6119.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
24	6119.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
25	6119.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
26	6119.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
27	6102.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
28	6102.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
29	4196	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
30	3851	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
31	3568	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
32	3343	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
33	3343	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
34	3327.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
35	3283	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
36	3248	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
37	3240	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
38	3240	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
39	3240	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
40	3240	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
41	3233.5	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
42	3225	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
43	3126	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
44	3126	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	
45	2792	MSKALLAVALWFVFETRAA.....KMYDAAVHADSGTTLRSPPV 1345	1345	ABM79009	

Query Match	100.0%	Score 7046; DB 7; Length 1345;	Qy	1021	KC1H3DLAARNLILSEKVNVKICFGGLARDIYKDPDYRKGDARLPLKRMAPETIFDRVY 1080
Best Local Similarity	100.0% ; Pred. No. 0;	Db	1021	KC1H3DLAARNLILSEKVNVKICFGGLARDIYKDPDYRKGDARLPLKRMAPETIFDRVY 1080	
Conservative	0; Mismatches	Db	1081	TIQSDVWSPGVLLMEI FSLGASPYPGVKIDEEF CRLKEGTRMADPTTPEMYQTMFLDC 1140	
Matches 1345;		Db	1081	TIQSDVWSPGVLLMEI FSLGASPYPGVKIDEEF CRLKEGTRMADPTTPEMYQTMFLDC 1140	
1 MESSKALIAVALWFCVERAASVGLTPHPPKLSLSTQDILTLANTLQITCRGORDLD 60		Qy	1141	WHEPNQRESFSELEVEHIGNLQNAQODGKDVTYLPSETLSMEEDSGSLSLPSPVSCM 1280	
1 MESSKALIAVALWFCVERAASVGLTPHPPKLSLSTQDILTLANTLQITCRGORDLD 60		Db	1141	WHEPNQRESFSELEVEHIGNLQNAQODGKDVTYLPSETLSMEEDSGSLSLPSPVSCM 1280	
61 WLWPNAQDSEBSERVLTTECGGGDSITPCKTLLTIPRVGNDTCAYKCSYRDVIASTYTY 120		Qy	1201	EEEVCDPKFHDTAGSHYLNQSKRSKRPVSKTFDIPLEPEVKVIPDDSQTDSCM 1280	
61 WLWPNAQDSEBSERVLTTECGGGDSITPCKTLLTIPRVGNDTCAYKCSYRDVIASTYTY 120		Db	1201	EEEVCDPKFHDTAGSHYLNQSKRSKRPVSKTFDIPLEPEVKVIPDDSQTDSCM 1280	
121 RDYRSPPIASVSDQHGVYTENQKTKVVI PGRGTSISLNLYSLCARYPERKFPDGNRIS 180		Qy	1261	VLASBELKTLEDRNKLSPSGGMPSPSKRSRESVSEGSNQTSGYGTHSDDDTDTVSSD 1320	
121 RDYRSPPIASVSDQHGVYTENQKTKVVI PGRGTSISLNLYSLCARYPERKFPDGNRIS 180		Db	1261	VLASBELKTLEDRNKLSPSGGMPSPSKRSRESVSEGSNQTSGYGTHSDDDTDTVSSD 1320	
181 WDSEIGFTLPSMISYAGMVPCEAKINDETYQSIMYI VVVGYRIVDVLSSPHEIELSA 240		Qy	1321	EAGLKKYMDAAVEADSGTLLRSPV 1345	
181 WDSEIGFTLPSMISYAGMVPCEAKINDETYQSIMYI VVVGYRIVDVLSSPHEIELSA 240		Db	1321	EAGLKKYMDAAVEADSGTLLRSPV 1345	
Qy	241 GEKLVNINCTARTELNVGLDFTWHSPPSKSHKKKIVNDRVKPFPGTVAKMPLSTTIEST 300				
Db	301 KSDQGEYTCVASSGRMKIKRNTFVYTHKEPIAFSGGMSLVEATVGSOVIRPKLSSP 360		RESULT 2		
Db	301 KSDQGEYTCVASSGRMKIKRNTFVYTHKEPIAFSGGMSLVEATVGSOVIRPKLSSP 360		ID ABR40197		
Qy	361 APDIKWRNGRPIESNYTMIVGDELTIMEYTERDAGNTVTLTNPISMKEQSHMVSLLVN 420		ID ABR40197 standard; protein; 1367 AA.		
Db	361 APDIKWRNGRPIESNYTMIVGDELTIMEYTERDAGNTVTLTNPISMKEQSHMVSLLVN 420		XX ABR40197;		
Qy	421 VPPQIGEKALISPMDSYQYGMQTLTCTTYANPLHIIQYQWOLEBACSYRPGQTSPVAC 480		AC AC		
Db	421 VPPQIGEKALISPMDSYQYGMQTLTCTTYANPLHIIQYQWOLEBACSYRPGQTSPVAC 480		XX DT 01-AUG-2003 (first entry)		
Qy	481 KEWRHVEDFOQGQNKLEVTRNQYALLEGKNTVSTVLIQANVNSALYKCEAINKAGRGRV 540		XX DE Murine vascular endothelial growth factor receptor-2.		
Db	481 KEWRHVEDFOQGQNKLEVTRNQYALLEGKNTVSTVLIQANVNSALYKCEAINKAGRGRV 540		XX DE Murine vascular endothelial growth factor receptor-2; cytostatic;		
Qy	541 ISFHVTRGPEITVQPAQPEQESVSLCPTADRNFTENLTWYKLGSQATSVMGESLTPV 600		XX KW angiogenic; antiangiogenic; antiarthritis; antirheumatic; antisense;		
Db	541 ISFHVTRGPEITVQPAQPEQESVSLCPTADRNFTENLTWYKLGSQATSVMGESLTPV 600		XX KW VEGFR-2; hyperproliferative disorder; cancer; rheumatoid arthritis;		
Qy	601 CKNLDAWKLNGMTMSNSTDNLIVAFQNALQDQGDYVCSAQDKKTKKRHCLVQQLLIL 660		XX KW angiogenesis.		
Db	601 CKNLDAWKLNGMTMSNSTDNLIVAFQNALQDQGDYVCSAQDKKTKKRHCLVQQLLIL 660		OS Mus musculus.		
Qy	661 ERMAPMTGLENQFTTIGETIVTCAGNCVGLCARAETLPIEGQETKNTLEVILVGTAVIAMFWIL 720		XX WO2003029266-A1.		
Db	661 ERMAPMTGLENQFTTIGETIVTCAGNCVGLCARAETLPIEGQETKNTLEVILVGTAVIAMFWIL 720		XX PN WO2003029266-A1.		
Qy	721 TIRRTRKEDGGLTCAOCHVGLCARAETLPIEGQETKNTLEVILVGTAVIAMFWIL 780		XX PD 10-APR-2003.		
Db	721 TIRRTRKEDGGLTCAOCHVGLCARAETLPIEGQETKNTLEVILVGTAVIAMFWIL 780		XX PF 26-SEP-2002; 2002WO-US030734.		
Qy	781 VIVLRTVKRANEGERLKTGYLSIVMDPDLDERCRLPYDASKWEPDRLKKGPKLGR 840		XX PR 28-SEP-2001; 2001US-00967655.		
Db	781 VIVLRTVKRANEGERLKTGYLSIVMDPDLDERCRLPYDASKWEPDRLKKGPKLGR 840		XX PA (ISIS-1 ISIS PHARM INC.		
Qy	841 GAFGQVIAADAFIDKTAETCKTAVKMLKEGATHSEHRLMSLKLHIGHLNVNL 900		XX PI Bennett CF, Watt AT;		
Db	841 GAFGQVIAADAFIDKTAETCKTAVKMLKEGATHSEHRLMSLKLHIGHLNVNL 900		XX WPI; 2003-371980/35.		
Qy	901 GACTKPGPGLMIVYBFCFKFGNLSTYLRGKNEFVYKSKGARFQGQYGEISLPLKRR 960		XX DR N-FSDB; ACC71720.		
Db	901 GACTKPGPGLMIVYBFCFKFGNLSTYLRGKNEFVYKSKGARFQGQYGEISLPLKRR 960		XX PT New compounds, particularly antisense oligonucleotides targeted to a		
Qy	961 LDSITSSQASSGGTVEKSLSDYEEERASEEELYKDFLTLHELYCISYFQVAKGMEFLASR 1020		PT nucleic acid encoding vascular endothelial growth factor receptor-2 (VEGFR-2) nucleotide sequence, and		
Db	961 LDSITSSQASSGGTVEKSLSDYEEERASEEELYKDFLTLHELYCISYFQVAKGMEFLASR 1020		PT which inhibit the expression of VEGFR-2. The oligonucleotides are useful		
Qy	961 LDSITSSQASSGGTVEKSLSDYEEERASEEELYKDFLTLHELYCISYFQVAKGMEFLASR 1020		CC in compositions for treating a disease or condition associated with VEGFR-2, such as hyperproliferative disorder, e.g. cancer, a disease or		
Db	961 LDSITSSQASSGGTVEKSLSDYEEERASEEELYKDFLTLHELYCISYFQVAKGMEFLASR 1020		CC condition involving angiogenesis, or rheumatoid arthritis. The present		
			CC sequence is murine VEGFR-2.		
			XX Example 13; Page 99-105; 127pp; English.		
			XX The present invention relates to novel antisense oligonucleotides		
			CC (AC7128-AC71250 and ACC80101-ACC80155) targeted to Vascular		
			CC Endothelial Growth Factor Receptor-2 (VEGFR-2) nucleotide sequence, and		
			CC which inhibit the expression of VEGFR-2. The oligonucleotides are useful		
			CC in compositions for treating a disease or condition associated with VEGFR-2, such as hyperproliferative disorder, e.g. cancer, a disease or		
			CC condition involving angiogenesis, or rheumatoid arthritis. The present		
			CC sequence is murine VEGFR-2.		
			XX XX XX		

Result No.	Score	Query	Match	Length	DB ID	Description
1	6998	99.3	1367	1	VGR2_MOUSE	P35918 mus musculu
2	6732	95.5	1343	1	VGR2_MOUSE	008775 rattus norv
3	6124.5	86.9	1356	1	VGR2_MOUSE	P35968 homo sapien
4	4810.5	68.3	1348	1	VGR2_MOUSE	P52583 coturnix co
5	2746.5	39.0	1363	1	VGR3_MOUSE	P35917 mus musculu
6	2694.5	38.2	1338	1	VGR3_MOUSE	P179438 hom. vascular
7	2677.5	38.0	1298	1	VGR3_MOUSE	P35916 hom. sapien
8	2606	37.0	1336	1	VGR1_MOUSE	P53767 rattus norv
9	2575	36.5	1333	1	VGR1_MOUSE	P20786 mus musculu
10	1162.5	16.5	1088	1	PDGS_RAT	P20786 rattus norv
11	1162	16.5	1089	1	PDGS_HUMAN	P16234 homo sapien
12	1146	16.3	1089	1	PDGS_MOUSE	P26618 mus musculu
13	1130.5	16.0	1087	1	PDGS_XENLA	P26619 xenopus lae
14	1043.5	14.8	960	1	KIT_CHICK	Q08156 gallus gall
15	1019.5	14.5	976	1	KIT_HUMAN	P10701 homo sapien
16	1019	14.5	1106	1	PDGR_HUMAN	P05619 homo sapien
17	1016.5	14.4	975	1	KIT_MOUSE	P05512 mus musculu
18	1013.5	14.4	978	1	KIT_CAPI	Q28317 capra hircu
19	1011	14.3	1097	1	PDGR_BAT	Q05030 rattus norv
20	1009	14.3	977	1	KIT_BOVIN	P43411 bos taurus
21	1005	14.3	978	1	KIT_PBLCA	Q28859 felis silve
22	1003	14.2	806	1	CBR2_CHICK	P18440 gallus gall
23	1002.5	14.2	819	1	FCR1_CHICK	P21844 gallus gall
24	1000.5	14.2	1098	1	FCR1_MOUSE	P05622 mus musculu
25	994	14.1	980	1	KFMS_PBLCA	P13349 felis silve
26	992	14.1	821	1	KFBS_MOUSE	P21843 mus musculu
27	990.5	14.1	972	1	KFMS_HUMAN	P07333 homo sapien
28	990	14.1	975	1	KIT_CANFA	Q97759 canis famil
29	986	14.0	822	1	FCR1_MOUSE	P16032 mus musculu
30	985	14.0	822	1	FGR1_HUMAN	P11342 homo sapien
31	984	14.0	822	1	FGR2_HUMAN	P21842 homo sapien
32	979	13.9	978	1	KFMS_FSVMD	P00545 feline sarc
33	976.5	13.9	812	1	FGR1_XENLA	P22162 xenopus lae

ALIGNMENTS						
RESULT 1						
ID	VGR2_MOUSE	STANDARD;	PRT;	1367 AA.		
AC	P35918;					
DT	01-JUN-1994	(Rel. 29, Created)				
DT	01-JUN-1994	(Rel. 29, Last sequence update)				
DT	10-OCT-2000	(Rel. 42, Last annotation update)				
DB	Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)					
DB	(VEGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase 1) (Kinase NYK)					
GN	KDR OR FLK1 OR FLK-1.					
OS	Mus musculus (Mouse)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus .					
NCBI_TaxID	100900;					
RN						
RP	SEQUENCE FROM N.A.					
RC	STRAIN=BALB/C; TISSUE=Embryo;					
RX	MEDLINE=93208880; PubMed=7681362;					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=CH/He; TISSUE=Fetal liver;					
RX	MEDLINE=9202084; PubMed=1717995;					
RP	"High affinity VEGF binding and developmental expression suggest RT					
RT	FLK1 as a major regulator of vasculogenesis and angiogenesis."					
RL	Cell 72:835-846 (1993).					
RN						
RP	SEQUENCE FROM N.A.					
RC	STRAIN=CH/He; TISSUE=Fetal liver;					
RX	MEDLINE=9202084; PubMed=1717995;					
RP	Mathews W., Jordan C.T., Gavin M., Jenkins N.A., Copeland N.G., Lemischka I.R.;					
RA	RA					
RT	"NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from a population of E10 embryonic neuroepithelial cells and exhibiting close genetic linkage to c-kit".					
RT	RT					
RL	Proc. Natl. Acad. Sci. U.S.A. 88:9026-9030(1991).					
RN						
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=93141255; PubMed=8423988;					
RA	Oelrichs R.B., Reid H.H., Bernard O., Ziemiczki A., Wilks A.F.;					
RT	"NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from a population of E10 embryonic neuroepithelial cells and exhibiting close genetic linkage to c-kit".					
RT	RT					
RN	Oncogene 8:11-18(1993).					
RP	SEQUENCE FROM N.A.					
RN	SEQUENCING OF 1-15 FROM N.A.					
RP	MEDLINE=96032749; PubMed=7559454;					
RP	Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E., Harber E.;					
RT	"Cloning and functional analysis of the promoter for KDR/Flk-1, a receptor for vascular endothelial growth factor.";					
RT	J. Biol. Chem. 270:23111-23118(1995).					
RN						
RP	FUNCTION.					
RX	MEDLINE=93361481; PubMed=8356051;					
RA	Quinn T.P., Peters K.G., de Vries C., Ferrara N., Williams L.T.;					
RT	"Fetal liver kinase 1 is a receptor for vascular endothelial growth factor and is selectively expressed in vascular endothelium."					
RT	RT					

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Om protein - protein search, using sw model

Run on: July 29, 2004, 13:33:52 ; Search time 51 Seconds
 8321.019 Million cell updates/sec
 (without alignments)

Title: US-10-090-183-6

Perfect score: 7046

Sequence: 1 MESSKALLAVALWFCVETRAA.....KIVDAAVHADSGTTLRSPPV 1345

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL_25:

1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_rhinc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rrodent:
 12: sp_rvirus:
 13: sp_vertebrate:
 14: sp_unclassified:
 15: sp_rvirus:
 16: sp_bacteriap:
 17: sp_archeap:

SPREMBL_25:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_rhinc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rrodent:
 12: sp_rvirus:
 13: sp_vertebrate:
 14: sp_unclassified:
 15: sp_rvirus:
 16: sp_bacteriap:
 17: sp_archeap:

17 1135 16.1 1062 13 Q8AXC7 fugu rubrip
 18 1134 16.1 976 13 Q8JTR5
 19 1133.5 16.1 1087 13 Q7ZT71
 20 1132 16.1 1059 13 Q9d449 brachydanio
 21 1128.5 16.0 453 11 Q9cm58 xenopus lae
 22 1128 16.0 984 13 Q8AXC6 mus musculu
 23 1114.5 15.8 1087 13 Q9PUF6 fugu rubrip
 24 11097 15.6 207 6 Q9N112 ovis aries
 25 1089 15.5 992 13 Q8AXU0 oncorhynchus
 26 1077.5 15.5 975 13 P79750 fugu rubrip
 27 1075.5 15.3 1474 5 Q8T4M0 drosophila
 28 1074 15.2 1503 5 Q8T4L8 drosophila
 29 1065 15.1 1509 5 Q95P10 drosophila
 30 1064 15.1 1509 5 Q8iPG1 drosophila
 31 1049.5 14.9 1048 13 P79749 fugu rubrip
 32 1049 14.9 1509 5 Q9VLQ8 drosophila
 33 1045 14.8 1461 5 Q8t9E6 drosophila
 34 1040.5 14.8 977 13 Q98SU2 danio kerri
 35 1037.5 14.7 977 13 Q98SU4 danio albol
 36 1037 14.7 974 13 Q98SU3 danio dangi
 37 1034.5 14.7 977 13 Q98SU1 danio nigro
 38 1033.5 14.7 977 13 Q91NG fugu rubrip
 39 1027.5 14.6 986 13 Q8UVR9 fugu rubrip
 40 1026.5 14.6 979 11 Q8C9K9 mus musculu
 41 1023.5 14.5 975 11 Q7t586 fugu rubrip
 42 1023.5 14.5 1019 13 Q8UVR8 fugu rubrip
 43 1023 14.5 445 5 Q9U8U8 branchiostoto
 44 1019 14.5 974 11 Q63702 rattus rattus
 45 1019 14.5 978 11 Q63116 rattus norvegicus

ALIGNMENTS

RESULT 1
 Q8VCD0 ID Q8VCD0, PRELIMINARY;
 AC Q8VCD0; DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-WAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DB Kinase insert domain protein receptor.
 GN KDR.
 OS Mus musculus (Mouse).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID:10090;
 OC RN [1]

SEQUENCE FROM N.A.
 RP TISSUE-Kidney;
 RC STRASBURG R.;
 RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RL -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY)
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 DR EMBL; BCO20530; AAH20530.1; -.
 DR MGD; MG_96683; Kar.
 DR GO:0045165; Picell fate commitment; IMP.
 DR InterPro; IPR03710; Ig-like.
 DR InterPro; IPR03598; Ig-c2.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR01824; ReceptykrknsIII.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_pk kinase_AS.
 DR Pfam; PF0047; Ig.
 DR Pfam; PF0069; kinase_1.
 DR ProDom; PD000001; Prot_kinase_2.
 DR SMART; SM00408; IgC2_1.
 DR SMART; SM00239; TyrKc_1.
 DR PROSITE; PS50835; Ig_LIKE_5.
 DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Query	Match	Length	DB	ID	Description
1	7040	99.9	1345	11	Q8VCD0	Q8VCD0 mus musculu	
2	2913	41.3	1379	13	P79701	P79701 coturnix coqui	
3	2730.5	38.8	1363	11	Q91ZT1	Q91ZT1 rattus norvegicus	
4	2666	37.8	1363	4	Q86W07	Q86W07 homo sapien	
5	2661.5	37.8	1298	4	Q86W08	Q86W08 homo sapien	
6	2639.5	37.5	1327	13	Q8QHL3	Q8QHL3 gallus gallus	
7	2495.5	35.4	1301	13	Q8UW9	Q8UW9 brachydanio	
8	2493	35.4	1302	13	Q8AXB3	Q8AXB3 brachydanio	
9	2357.5	33.5	1173	13	Q9PTL0	Q9PTL0 brachydanio	
10	2210.5	31.4	1092	11	Q91ZT0	Q91ZT0 rattus norvegicus	
11	1796	25.5	341	11	Q8CD05	Q8CD05 mus musculu	
12	1322.5	18.8	346	13	Q425T0	Q425T0 xenopus laevis	
13	1172	16.6	287	13	Q42377	Q42377 brachydanio	
14	1154.5	16.4	1078	13	Q8AXC8	Q8AXC8 fugu rubripinnis	
15	1150	16.3	1089	11	Q7TSU3	Q7TSU3 mus musculu	
16	1135	16.1	976	13	Q9W755	Q9W755 brachydanio	

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: August 6, 2004, 10:44:22 ; Search time 247 Seconds

(without alignments)
12110.062 Million cell updates/sec

Title: US-10-090-183-5

Perfect score: 5390

Sequence: 1 ctgtgtccggccggata tctgcctgtgtctatgtt 5390

Scoring table: IDENTITY NUC

Gapcost 10.0 , Gapext 1.0

Searched: 682709 seqs, 27475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A COMB. seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB. seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB. seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB. seq.*
5: /cgn2_6/ptodata/2/ina/PTUS COMB. seq.*
6: /cgn2_6/ptodata/2/ina/backflesi. seq.*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
1	5346	99.2	5470	2	US-08-443-861-1	Sequence 1, Appli
2	5346	99.2	5470	3	US-08-193-029B-1	Sequence 1, Appli
3	5336.8	99.0	5406	1	US-07-813-593-3	Sequence 3, Appli
4	5336.8	99.0	5406	1	US-07-977-451-5	Sequence 5, Appli
5	5336.8	99.0	5406	1	US-07-946-507-3	Sequence 3, Appli
6	5336.8	99.0	5406	1	US-08-252-517-5	Sequence 5, Appli
7	5336.8	99.0	5406	1	US-07-906-397A-5	Sequence 5, Appli
8	5336.8	99.0	5406	1	US-08-601-891-5	Sequence 5, Appli
9	5336.8	99.0	5406	2	US-09-021-324-5	Sequence 5, Appli
10	5336.8	99.0	5406	4	US-09-098-136B-5	Sequence 5, Appli
11	5336.8	99.0	5406	5	PCT-US92-0750-7	Sequence 7, Appli
12	5336.8	99.0	5406	5	PCT-US92-05401-5	Sequence 5, Appli
13	5336.8	99.0	5406	5	PCT-US92-05893-5	Sequence 5, Appli
14	3066.8	56.9	4236	1	US-08-810-116-7	Sequence 7, Appli
15	3066.8	56.9	4236	2	US-07-930-548A-7	Sequence 7, Appli
16	3024.6	56.1	4071	3	US-09-098-707A-1	Sequence 1, Appli
17	3024.6	56.1	4071	4	US-09-483-539-1	Sequence 1, Appli
18	2412.4	44.8	2431	3	US-08-985-526-35	Sequence 35, Appli
19	1656.8	30.7	2383	1	US-08-232-538-18	Sequence 18, Appli
20	1656.8	30.7	2383	2	US-08-786-164-18	Sequence 1, Appli
21	1592.4	29.5	2292	4	US-09-142-956B-1	Sequence 16, Appli
22	1420	26.3	2264	1	US-08-232-538-16	Sequence 16, Appli
23	1420	26.3	2264	2	US-08-786-164-16	Sequence 5, Appli
24	768	14.2	4014	4	US-08-119-014D-5	Sequence 244, App
25	757	14.0	7718	4	US-08-976-594-244	Sequence 1, Appli
26	716.2	13.3	4195	1	US-08-340-011-1	Sequence 1, Appli
27	716.2	13.3	4195	3	US-08-901-710-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1	US-08-443-861-1	Sequence 1, Application US/08443861
		Patent No. 585199
		GENERAL INFORMATION:
		APPLICANT: Ullrich, Axel
		APPLICANT: Rissau, Werner
		APPLICANT: Millauer, Birgit
		APPLICANT: Gavit, Aviv
		APPLICANT: Levitzki, Alex
		TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular
		TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular
		NUMBER OF SEQUENCES: 6
		CORRESPONDENCE ADDRESS:
		ADDRESSEE: Pennie & Edmonds
		STREET: 1155 Avenue of the Americas
		CITY: New York
		STATE: New York
		COUNTRY: U.S.A.
		ZIP: 10036-2711
		COMPUTER READABLE FORM:
		MEDIUM TYPE: Floppy disk
		COMPUTER: IBM PC compatible
		OPERATING SYSTEM: PC-DOS/MS-DOS
		SOFTWARE: Patent Release #1.0, Version #1.25
		CURRENT APPLICATION DATA:
		APPLICATION NUMBER: US/08/443,861
		FILING DATE: 22-MAY-1995
		CLASSIFICATION: 514
		PRIOR APPLICATION NUMBER: 514
		APPLICATION NUMBER: US 08/193,829
		FILING DATE: 09-FEB-1994
		ATTORNEY/AGENT INFORMATION:
		NAME: Coruzzi, Laura A.
		REGISTRATION NUMBER: 30,742
		SEQUENCE/DOCKET NUMBER: 7683-060
		TELECOMMUNICATION INFORMATION:
		TELEPHONE: (212)790-9090
		TELEFAX: (212)865-9741
		TELEX: 66141 PENNIE
		INFORMATION FOR SEQ ID NO: 1:
		SEQUENCE CHARACTERISTICS:
		LENGTH: 5470 base pairs
		TYPE: nucleic acid
		STRANDEDNESS: unknown
		TOPOLOGY: unknown
		MOLECULE TYPE: DNA
		FEATURES:
		NAME/KEY: CDS
		LOCATION: 286..4386

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 10:44:22 ; Search time 8373 Seconds
(without alignments)

19223.355 Million cell updates/sec

Title: US-10-090-183-5

Perfect score: 5390

Sequence: 1 ctgtgtcccgaggccgata.....tctgcctgtgtgtatgtt 5390

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0* Maximum Match 100* Listing first 45 summaries

Database : BST:+

1: em_estba:*

2: em_estbum:*

3: em_estin:*

4: em_estmu:*

5: em_estcov:*

6: em_estcp1:*

7: em_estro:*

8: em_hrc:*

9: gb_est1:*

10: 9b_est2:*

11: 9b_hrc:*

12: 9b_est3:*

13: 9b_est4:*

14: 9b_est5:*

15: em_estfun:*

16: em_estom:*

17: em_g88_hum:*

18: em_g88_irv:*

19: em_g88_pln:*

20: em_g88_vrt:*

21: em_g88_fun:*

22: em_g88_man:*

23: em_g88_mms:*

24: em_g88_pro:*

25: em_g88_rnd:*

26: em_g88_phg:*

27: em_g88_vrt:*

28: 9b_g88i:*

29: 9b_g982:*

5 751.8 13.9 816 12 BI081886 602877109

6 750.6 13.9 835 12 BI731060 603351683

7 730.2 13.5 896 14 CB849137 MRA-0816

8 716.2 13.3 948 13 B0714332 AGENCOURT

9 712 13.2 724 13 BQ572655 UI-M-FDO-

10 702.4 13.0 748 14 CP539944 UI-M-EXO-

11 685.4 12.7 857 14 CD107886 AGENCOURT

12 674 12.5 751 14 CR512955 UI-R-FJO-

13 658.2 12.2 1067 12 BM925760 AGENCOURT

14 653 12.1 786 14 CR463143

15 636.4 11.8 697 12 BM93389 UI-M-EQO-

16 630.2 11.7 729 12 BGB63384 603797010

17 629.6 11.7 1195 9 AL550235 AL550235

18 626 11.6 953 13 BQ946333 AGENCOURT

19 609.2 11.3 656 10 BB577273 BB577273

20 600 11.1 600 14 CA527179 8032-85 M

21 586.8 10.9 924 10 BF098937 60120434

22 580.2 10.8 689 9 AA122701 mo3dd07.r

23 574 10.6 3751 29 AY404031 Homo sapi

24 570 10.6 3559 29 AY404032 Pan trogl.

25 567.2 10.5 659 9 AA033284 mi4dd09.r

26 563.2 10.4 675 10 BB287063 60109108

27 554.6 10.3 645 10 BE336067

28 522.4 9.8 553 12 BM248779 K0822C02-

29 526.6 9.8 627 10 BF302717 602032587

30 526 9.8 763 10 BF784985 60311095

31 522.2 9.7 723 14 CD806166 UI-M-GW0-

32 509.4 9.5 563 14 CB609012 AMGNNUC.S

33 503 9.3 709 9 AI325028 mo3dd07.r

34 504.6 9.3 556 14 CB613414 AMGNNUC.M

35 498.2 9.2 3754 29 AY404033 Mus musculu

36 479.4 8.9 623 10 BF087455 PM1-P-CPA-

37 470.6 8.7 701 13 BQ603967 BE916077

38 461 8.6 919 10 BE916077

39 451.6 8.4 974 11 BIS99221 603250231

40 448.6 8.3 711 14 CP109220 Shultz zom

41 444 8.2 807 14 CD656643 AGENCOURT

42 441.4 8.2 443 13 BY544133

43 437.2 8.1 477 14 W85664 mF42all.r1

44 436.2 8.1 765 12 BI823988 603039184

45 435.4 8.1 487 14 CB726482 AMGNNUC.N

ALIGNMENTS

RESULT 1 AK031739 LOCUS Mus musculus 14 days embryo thymus cDNA, RIKEN full-length enriched library, clone:6130401c07 receptor, full insert sequence.

DEFINITION AK031739.1 HTC: CAP trapper.

ACCESSION AK031739.1

VERSION HTC

KEYWORDS SOURCE Mus musculus (house mouse)

ORGANISM Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bularyota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE Carninci, P. and Hayashizaki, Y.

AUTHORS High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

AUTHORS Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 2099374

PUBMED 11042159

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.06	39.1	2612	11 AK031739	
2	15.66	29.1	3176	11 AK054510	
3	816.2	15.1	868	14 CR979203	
4	765.6	14.2	809	13 BUT079245	

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OM nucleic - nucleic search, using bw model

Run on: August 6, 2004, 10:44:22 ; Search time 1229 Seconds (without alignment(s)) 18631.235 Million cell updates/sec

Title: US-10-090-183-5

Perfect score: 5390

Sequence: 1 ctgtgtcccgaggccgata.....tctgcccgtgtgtatgtt 5390

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0[‡]
Maximum Match 100[‡]
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: geneseqm1980s:*

2: geneseqm1990s:*

3: geneseqm2000s:*

4: geneseqm2001as:*

5: geneseqm2001bs:*

6: geneseqm2002as:*

7: geneseqm2003as:*

8: geneseqm2003bs:*

9: geneseqm2003cs:*

10: geneseqm2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	5390	100.0	5390	9	ACF80603		Act80603 Murine Flk
2	5346	99.2	5470	7	ACCF7120		Acc7120 Murine va
3	5336.8	99.0	5406	2	AA040916		Aa040916 Murine fl
4	5336.8	99.0	5406	2	AA053504		Aa053504 Murine fl
5	5336.8	99.0	5406	2	AA079070		Aa079070 Mouse flk
6	5336.8	99.0	5406	2	AA081014		Aa081014 Flk1 recce
7	5336.8	99.0	5406	2	AA72119		Aa72119 Murine fl
8	5336.8	99.0	5406	6	AB55046		Ab55046 Mouse cDN
9	5335.2	99.0	5406	2	AAQ35251		Aaq35251 Human flk
10	5331.6	98.9	5470	2	AA064049		Aa064049 Sequance
11	5330.4	98.9	5406	2	AAQ29957		Aaq29957 Flk-1 cDN
12	5322.8	98.8	5404	2	AA738735		Aa738735 Murine fo
13	5322.8	98.8	5404	2	AAK77516		Aak77516 Murine fl
14	5074.8	94.2	5363	6	AA042485		Aa042485 Murine re
15	4259	79.0	5892	9	AB58183		Ab58183 Toxicity-
16	3354.4	62.2	5832	8	ACR03813		Acr03813 Human cDN
17	3317.8	61.6	5330	7	ACCT7113		Acct7113 Human vas
18	3316.2	61.5	5330	9	ADD08953		Ad08953 Human VEG
19	3081.2	57.2	4225	4	AAF83308		Aaf83308 Human VEG
20	3066.8	56.9	4236	2	AAV734763		Aav734763 Human KDR
21	3027.8	56.2	4071	6	ABV78213		Abv78213 Human KDR
22	3027.8	56.2	4071	6	ABZ35789		Abz35789 Human KDR
23	3027.8	56.2	4071	6	ABX10032		Abx10032 Human KDR

RESULT 1

ACF80603	ID	ACF80603	standard; cDNA; 5390 BP.
XX	AC	ACF80603;	
XX	XX		
15-JAN-2004	DT		(First entry)
XX	DB		Murine Flk-1 coding sequence.
XX	XX		
Mouse; vascular endothelial growth factor; receptor; Flk-1; vaccine; gene; ss.	XX		
XX	OS		
OS	SP		
XX	Key		Location/Qualifiers
FT	CDS		208..4347
FT			/*tag= a
FT			/product= "Mouse Flk-1"
XX	XX		
PN	W02003073995-A2.		
XX	XX		
PD	12-SEP-2003.		
XX	XX		
XX	XX		PP 28-FEB-2003 ; 2003WO-US006256.
XX	XX		PR 02-MAR-2002 ; 2002US-00090183.
XX	XX		(SCRI) SCRIPPS RES INST.
PA	PA		
XX	XX		PI Reisfeld RA, Niethammer AG, Xiang R;
XX	XX		DR WPI ; 2003-756753/71.
XX	XX		DR P-PSDB; ABM79009.
XX	XX		PT New DNA vaccine for eliciting an immune response against proliferating endothelial cells comprising a DNA construct operably encoding a VEGF receptor protein in a carrier, useful for inhibiting tumor growth or angiogenesis.
XX	XX		PT
PS	PS		PT
XX	XX		CC The present sequence is the coding sequence for murine Flk-1, an endothelial growth factor receptor protein. A claimed DNA vaccine effective for eliciting an immune response against proliferating endothelial cells comprises a DNA construct operably encoding a VEGF
CC	CC		CC
CC	CC		CC
CC	CC		CC

ALIGNMENTS

GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 10:44:22 ; Search time 13494 Seconds
(without alignments)
17312.802 Million cell updates/sec

Title: US-10-090-183-5
Perfect score: 5390
Sequence: 1 ctgtgtccgcagccggata.....tctgctgtgtgtatgtt 5390

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:
1: 9b_ba:/*
2: 9b_ng:/*
3: 9b_im:/*
4: 9b_cm:/*
5: 9b_ov:/*
6: 9b_dat:/*
7: 9b_ph:/*
8: 9b_pl:/*
9: 9b_pr:/*
10: 9b_ro:/*
11: 9b_sts:/*
12: 9b_sy:/*
13: 9b_un:/*
14: 9b_ir:/*
15: em_ba:/*
16: em_fun:/*
17: em_num:/*
18: em_in:/*
19: em_mu:/*
20: em_on:/*
21: em_or:/*
22: em_ov:/*
23: em_dat:/*
24: em_ph:/*
25: em_pl:/*
26: em_ro:/*
27: em_sts:/*
28: em_un:/*
29: em_v1:/*
30: em_htg_hum:/*
31: em_htg_inv:/*
32: em_htg_other:/*
33: em_htg_mus:/*
34: em_htg_pln:/*
35: em_htg_rdn:/*
36: em_htg_mam:/*
37: em_htg_vrt:/*
38: em_sy:/*
39: em_htgo_hum:/*
40: em_htgo_mus:/*
41: em_htgo_other:/*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	5366.2	99.6	5391	10	MMFLKL	X59397 Mouse Flk-1
2	5346	99.2	5470	6	AR068047	AR068047 Sequence
3	5346	99.2	5470	6	AR125518	AR125518
4	5346	99.2	5470	10	MMFLKL	X70842 M.musculus
5	5336.8	99.0	5406	6	AR005213	AR005213 Sequence
6	5336.8	99.0	5406	6	AR071705	AR071705 Sequence
7	5336.8	99.0	5406	6	I25171	I25171 Sequence 5
8	5336.8	99.0	5406	6	I40602	I40602 Sequence 5
9	5219.6	98.0	5464	10	BC026530	Mus musculus
10	4557.2	86.4	4790	10	SS3103	SS3103 NYK/FLK-1
11	4259	79.0	5892	10	RNU93306	U93306 Rattus norvegicus
12	3317.8	61.6	5830	6	AX743112	AX743112 Sequence
13	3317.8	61.6	5830	9	AF035121	Homo sapiens
14	3081.2	57.2	4225	6	AX133339	AX133339 Sequence
15	3066.8	56.9	4236	6	AR030758	AR030758 Sequence
16	3060.8	56.8	4230	9	HSGFRX	X61656 H.sapiens
17	3060.8	56.8	4230	9	HUMKDRZ	LO947 Homo sapiens
18	3027.8	56.2	4071	6	AX481483	AX481483 Sequence
19	3027.8	56.2	4071	9	AF063658	Homo sapiens
20	3026.2	56.1	4044	6	AX481480	AX481480 Sequence
21	3024.6	56.1	4071	6	AR14203	AR14203 Sequence
22	3024.6	56.1	4071	6	AR20182	AR20182 Sequence
23	3024.6	56.1	4071	6	BD132942	BD132942 Human rec
24	2728	50.6	4016	10	RNU93307	U93307 Rattus norvegicus
25	2412.4	44.8	2431	6	AR100641	AR100641 Sequence
26	2412.4	44.8	2431	6	E34072	E34072 Carrier/DNA
27	1904.8	35.3	5390	5	X83288	C.coturnix
28	1753.8	32.5	2555	6	A64406	A64406 Sequence 19
29	1656.8	30.7	2383	6	AR030850	AR030850 Sequence 18
30	1656.8	30.7	2383	6	182809	182809 Sequence 18
31	1621.6	30.1	3009	6	AX060542	AX060542 Sequence
32	1592.4	29.5	2292	6	AR194072	AR194072 Sequence
33	1581.4	29.3	2281	6	AX133343	AX133343 Sequence
34	1420	26.3	2264	6	AR030448	AR030448 Sequence
35	1420	26.3	2264	6	I82807	I82807 Sequence 16
c	1279.2	23.7	221665	2	AC134903	AC134903 Mus musculus
37	810.6	15.0	4617	5	CCQBZ2	X83287 C.coturnix
38	768	14.2	4014	6	AR39797	AR39797 Sequence
39	768	14.2	4017	9	AX481481	AX481481 Sequence
40	768	14.2	4017	9	AF063657	AF063657 Homo sapiens
41	768	14.2	7680	9	XS1602	X51602 Human fit
42	727.8	13.5	2619	5	S65205	S65205 endothelial
43	727	13.5	4272	5	AB065372	AB065372 Gallus gallus
44	720.6	13.4	5284	10	MUSRKA	L07296 Mus musculus
45	717.8	13.3	3897	6	AX481482	AX481482 Sequence

ALIGNMENTS

RESULT 1	MMFLKL	MMFLKL	5391 bp mRNA linear
LOCUS	Mouse Flk-1	Mouse Flk-1	for a tyrosine kinase receptor.
DEFINITION	X59397	X59397	GI:50976
VERSION			
KEYWORDS	Flk-1 gene; tyrosine kinase receptor.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.		
REFERENCES	1 (bases 1 to 5391)		
AUTHORS	Matthews, W.; Jordan, C.T.; Gavin, M.; Jenkins, N.A.; Copeland, N.G. and Lemischka, I.R.		
TITLE	A receptor tyrosine kinase cDNA isolated from a population of		